

FIGURE 1

[illegible]

FIGURE 2

HIV	RT	VKLPGMDGPKVKVQ	WPLTEEKIKALVEICTEMEKECKISKICPENFYNTFVFAIKKCDSTKVR	
HTLV1	RT	RPWARTPPKAPKQV	PVPFKPERLQALQHLVRKALEACHIEPTYC	PGNNPVFPVKKA NGTVR
Ec-67	RT	NVLYRGISDNQYQTFIT	PKPKGCVRTISAPTDLR	KDIQRRCIDLLSDCRDEIFAIRKI SNNYS
Hx-162	RT	AFHREVDTATHYVSWTIP	KRDCGSKRTITSKPKEL KAAQR	VWLS NVV ERLP VHCAA
			o ooo o o x xx oo	o x
HIV	RT	KLVDFRELNKRTQDFVEV	QLGIPHAGLKKK KSVTVLVDGDAYFSVPLDEDFRKYT	A
HTLV1	RT	FIHDLRATNSLTLDLSSSS	PGPDLSSLPITLALHQTIDLRDAFFQIPLPKQFPQPYF	A
Ec-67	RT	FGFE	RCKSIILNAYKHRCQITILNIDLKDFESFNFCVRVG YFLS NQDF	L
Hx-162	RT	HGCV	ACRSILTNALAHQCADV	VVVKVLDLKFFPSTVTRRVKGLLRKGCLEGTSTILLSLLSTEAP
			oo o oo xx x o o xooooo xxx o x	x x
HIV	RT	FTIP	SINNETPGIRYQYNVLPGCKWGCSPAIFQS	SMTKILEPFKKQNPDIVIYQYHDDL
HTLV1	RT	FTIP	QOCNYGPGTRYAKVLP	QCFKNSPTLFEM QLAHLIQPIRQAFQPGCTILCYHDDILLLA
Ec-67	RT	LN	PVVATTLAKAACYN GTLPQCS	PCSPISNLICNIDHMR
Hx-162	RT	REAVQ	FRGKLLHVAKGP RALPQCA	PTSPGITHNALCLDKRLSALAKRL CFTYTR
			o o o o o o o o x x x x x	o x x
HIV	RT	S	DLEIGQHRTEIEELRQHLLRWGLTTP	DKKHQKEP PFLWMCYELHPDKVTVQPIVPE KD
HTLV1	RT	S	PSHEDLLLLSEATHSLISHLG	LPV ENKQTQPGTIKFGLQIISPHNLTYDAVPTPI RS
Ec-67	RT	STNK	TFPLEMATVQEGVGLKV	LKVEIENSGFEINDSKRLTYTSRQEV GTLVNRIVND
Hx-162	RT	SWTKAKQ	PKPRTRQRPVAVLLSRVQ	EVVEAEGFRVHPDKTRVARKGTRQRT GLVVNAAGKDA
			o o o o o o o x x x x x x	o x x
HIV	RT	SVTVNDI	QIKLVGKLNWASQIYP	
HTLV1	RT	RWALPEL	QALLGEIQWVS	GKTP
Ec-67	RT	RCYYK	KTRALAHALRYTGE	
Hx-162	RT	PAARVP	PDVVQRQLAAIHN	RK

FIGURE 3

A

Mx-162 18 PTPELTAPSSDAAAKREARRLAHEALLVRKAIDEAGGADDWVQAQLVSKGLAVEDLD-FSSASEKDKA-WKEKK 91

Mo-MLV 1070 PDPDMTRVTNSPSLQAHLQALYLVQHEVW-RPL-AAAYQEQ-LDRPVVPHPYRVGDTVWVRRHQTKNLEPRWKGPY 1142

Mx 162 92 KAEATERRALKRQAHEAW-KATHVGHLGAGVHWAEDRL 128

Mo-MLV 1143 TVLLTTPTALKVDGIAAWIHAHVKAADPGGG-PSSRL 1179

B

Mx-162 411 GKDAAPARVPRDVRQLRAAIHNRKKKPGREGESLEQLKGMAAFIMTD-PAKGRAF-LAQLTELESTASAAPQAE 485

HIV 396 GKEGHSARQCR-APR--RQGC--WKCKKPGHIMTNC PD-R-QAGFLGLGPNKPKPRNFPVAQVPQ-GLTPTAPP 461

Figure 4. Sequence Similarity of the msDNA-Mx162 Reverse Transcriptase with Other Retroelements

(A) Sequence similarity of the region from residues 18 to 128 of the msDNA Mx162 RT (see Figure 2) with a carboxy-terminal region of integration protein of Moloney murine leukemia virus (M-MuLV) (residues 1070 to 1179; Shinnick et al., 1981)

(B) Comparison of the sequence from residues 411 to 485 of the msDNA-Mx162 RT (see Figure 2) with the sequence from residues 396 to 461 of the gag protein of human immunodeficiency virus (HIV; Ratner et al., 1985).

FIGURE 4

A

Mx-162	304	GP-RALPQGAPSPGITHNALCLKDKRLSALAKRL-GFTYTRYADLTF-SWTKAKQPKPRRTQRPVAVL	371
Ec-67	159	YN-GTLPGQSPSPISNLICINDMRLAKLAKKY-GCTYSRYADLTI-STNKWTFPLEMATVQPEGVVL	226
Ec-86	130	YK-NLLPQGAPSSPKLANLICSKLDYRIQGYAGSR-GLIYTRYADLTL-SAQSMKKVVKARDFLFSIIPS	197
HIV	311	YQYNVLPQGWKGSPIAFQS---SMTKILEPFKKQNPDIYIYQYMDLLVGS-DLEIGQHRTKIEELRQHLL	377
HTLV1	150	YANKVLPQGFKNSTPLFEM---QLAHILQPIRQAFQCTILQYMDILLAS--PSHEDLLLSEATMASLI	215
Mo-MLV	303	LTWTRLPGGFKNSTPLFDE---ALHRDLADFRIQHPDLILLQYVDELLAA-TSELDCCQG-TRALL-QTL	367
RSV	141	FQWKVLPQGMTCSPTICQL---VVGQVLEPLRLKHPSLCMLHYMDLLAA--SSHGGLAAGEEVI-STL	205
BLV	122	FAWRVLPQGFINSALFER---ALQEPLRQVSAAFSQSLLVSYMDILYAS--PTEEQRSQCYQALA-ARL	186
Mt. plasmid	288	IATNGVPQGAFTSCGLATYNVL-----ELFLRY--DELIMYADDGIL-CRQDPSTPDFSVEEAGVVQEP	348
17.6	339	YEYLRMPFGLKNAP-ATFORCMN-DI---LRPLLKHC-LVYLDHIVFS-TSLDEHLQSLGLVFE--KL	399
GYPSY	284	YEFCLPFGLRNASSIFQR---ALDDV---LREQI-GKICYVVDVVIIFS--ENESDHVRHIDTVLK-CL	344
Copia	1032	CKLNKAIYGLKQAARCWFR-CIYI---LDKGNINENIYV-LLYVDVVIAT--GDMTRMNNFKRYLME-KF	1112
Tai-3	990	CLLKSLYGLKQSPQWNA-CVYV-KQVSE-QEHLYL---LLYVDDMLIAG--KSKSEINKVKEQLSM-EF	1069
Ty912	948	IRLKSLYELKQS-GANWYE--EVRG-WSCVFKNSQV-TICLFVDDHVLFS--KNLNSNKRIIEKLQM-QY	1023

B

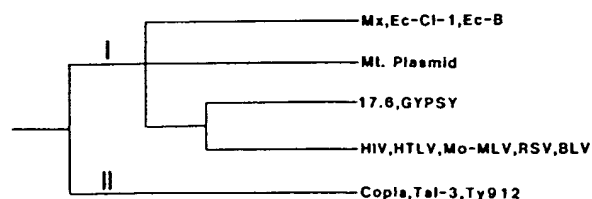


FIGURE 5

S 1 2 3 4



08808031-030397

FIGURE 6

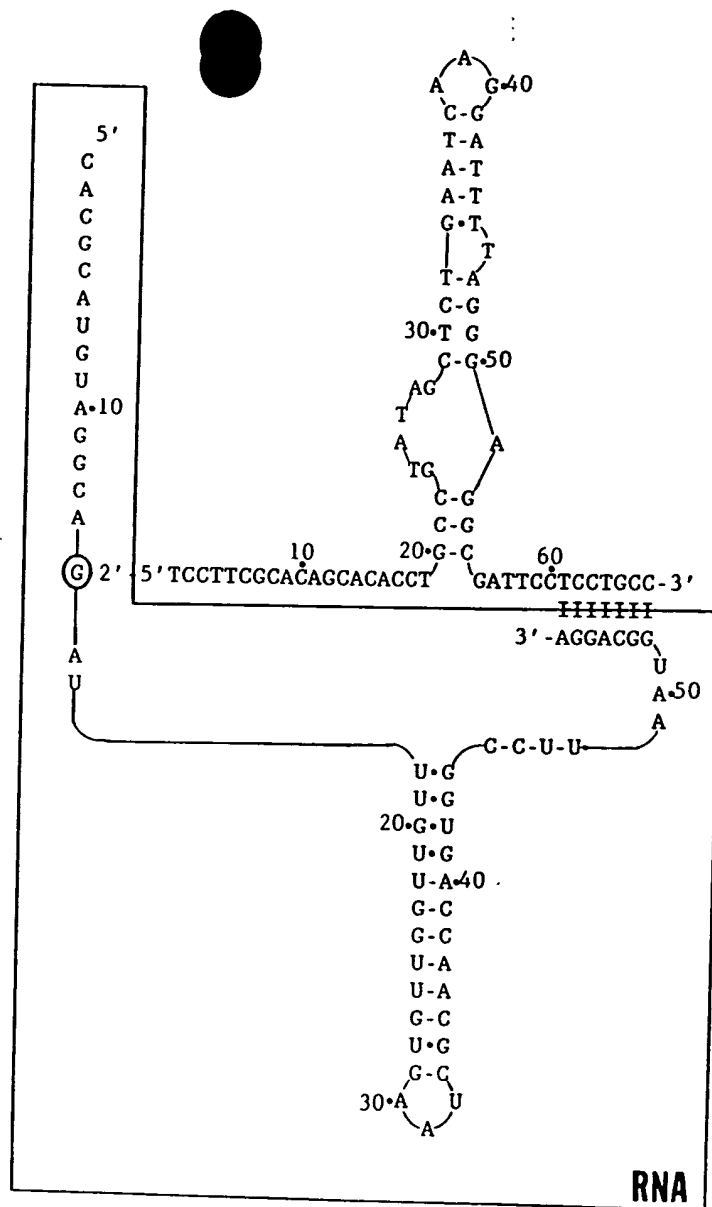
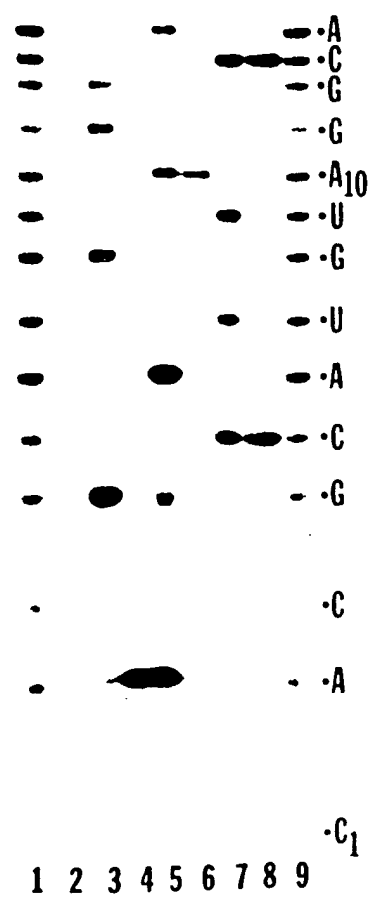


FIGURE 7

OH⁻ E T1 U2 U2 PhylM Bc CL3 OH⁻



$\cdot C_1$

FIGURE 9

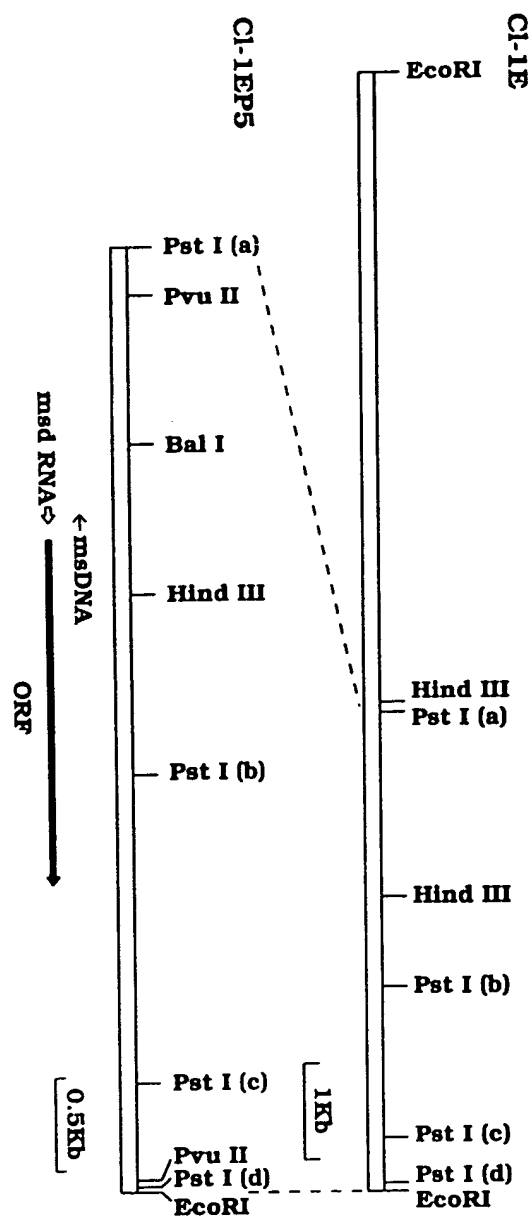


FIGURE 10

08808031-030397

TCG CCA TTT TCA GAT CTT TCA GAT CCG CCA GAA CTC GCG GCG TTT TCC TCA 170
GCA TGA TCG CCA GAT CTT TCA GAT CCG CCA GAA CTC GCG GCG TTT TCC TCA 180
TGT CAT CCA TGT CCA TCA AAA CCA CTC CAT AAA CCG GCG AGC CCG GCG GAT ACC ACC 180
CCG GCG TAT CAC CCA AAA TAG CCA AAA TAG TTC TCG AAA ACA GAA ACT TGA ACT GAT ATG 240
TTC ATA AAC ACC CAT CTA GCG CCA TTT CTT CTT TGT GAA TCG CAA CCA CTC GCG TTA ATG 300
AAG TAT TTC TCG CTA CAT CCG TCT AAA CAA CCA ACA CTT ACC GTT GGT CAC CCG AAT TAG
CGA GCA GCA ATG GCG TCG CTA AAA TCG TTG ATT CAG ACC TAT ACC GCA GGT CTC CTC TCG 360
CGT CCG CCG TAG GCG AGC GAT TTT AGC AAC TAA CTC TCG ATA TCG CCG CCA CAC GAC ACC
GAA GCA GTC CCG CCA TCG CTT TCT CCG CCG TTT TTC CTC TCG CAT GAA GAA GAA ATG 420
CTT CCG CAC GCA CCG ACC CAA AGA CCA ACC GCA AAA AAG GAG ACC CTA CTT CTT CTT TAC
ACA AAA ACA TCT AAA CTT GAC CCA CTT AGC GCT CCG ACT TCA CCG GAA GAC TTC GCT AAA 480
T K T S K L D A L R A A T S R E D L A K
ATT TTA CAT ATT AAG TTG GTA TTT TTA ACT AAC CTT CTA TAT AGA ATC CCG TCG CAT AAT 540
I L D I K L V F L T N V L Y R I C S D N
CAA TAC ACT CAA TTT ACA ATA CCG AAC AAA GCA AAA GCG GTA AGC ACT ATT TCT CCA CCG 600
Q Y T Q F T I P K K G K C V R T I S A P
ACA GAC CCG TTG AAG CAC ATC CAA CCA AGA ATA TGT GAC TTA CTT TCT GAT TGT AGA CAT 660
T D R L K D I Q R R I C D L L S D C R D
GAG ATG TTT GCT ATA ACC AAA ATT AGT AAC AAC TAT TCG TTT CCG TTT GAG AGC GCA AAA 720
E I F A I R K I S N N Y S F G F E R C K
TCA ATA ATC CTA AAT CCG TAT AAG CAT AGA CCG AAA CAA ATA ATA TTA AAT ATA GAT CTT 780
S I I L N A Y K H R G K Q I I L N I D L
AAG GAT TTT TTT CAA ACC TTT AAT TTT CCA CCA CTT ACA GCA TAT TTT CTT TCC AAT CAG 840
K D F F E S F N F G R V R G Y F L S N Q
GAT TTT TTA TTA AAT CCG CTC GTC CCA ACC ACA CTT CCA AAA CCG CCA TCG TAT AAT GCA 900
D F L L N P V V A T T L A K A A C Y N G
ACC CTC CCG CAA CCA AGT CCA TGT TCT CCG ATT ATC TCA AAT CTA ATT TCG AAT ATT ATG 960
Y L P Q G S P C S P I I S N L I C N I N
CAT ATG AGA TTA CCG ATG GCT AAA AAA TAT CCA TGT ACT TAT ACC GAT TAT CCG GAT 1020
D H R L A K L A K K Y G C T Y S R K A L
GAT ATA AGA ATT TCT ACA AAT AAA AAT AGA TTT CCG TTA CAA ATG CCG CTT CTC CAA CCG 1080
D I T I S T N K N T F P L E H A T V Q P
GAA CCG CTT CTT TTG CCA AAA CTT TTG GTA AAA CAA ATA CAA AAC TCT CCA TTC CAA ATA 1140
E G V V L G K V L V K E I E N S G F E I
AAT GAT TCA AAG ACT AGC CTT ACC TAT AAG ACA TCA ACC CAA GAA CTA ACC GCA CTT ACA 1200
N D S K T R L T Y K T S R Q E V Y G L T
GTT AAC AGA ATC CTT AAT ATT CAT AGA TGT TAT TAT AAA AAA ACT CCG CCG TTG CCA CAT 1260
V N R I V N I D R C Y Y K K T R A L A N
CGT TTG TAT CCG ACA CCG CAA TAT AAA CTC CCA CAT GAA AAT CCG CTT TTA CTT TCA GCA 1320
A L Y R T G E Y K V P D E H G V L V S C
CGT CTC GAT AAA CTT CAG CCG ATC TTT CCG TTT ATT CAT CAA CTT CAT AAG TTT AAC AAT 1380
G L D K L E C M F C F I D Q V D K F N N
ATA AAG AAA AAA CTC AAG AAC CCA CCG GAT AGA TAT CTA TTC ACT AAT CCG ACT TTG CAT 1440
I K K K L N K Q P D R Y V L T N A T L H
CGT TTT AAA TTA AAG TTG AAT CCG CCA GAA AAA GCA TAT ACT AAA TTT ATT TAC TAT AAA 1500
G F K L K L N A R E K A Y S K F I Y Y K
TTT TTT CAT CCG AAC ACC CCG CCG ACC ATA ATT ACA CAA CCG AAC ACT CAT CCG ATA TAT 1560
F F H G N T C P T I I T E C K T D R I Y
TTG AAG CCG CCG TTG CAT TCT TTG GAG ACA TCA TAT CCG CAG TTG TTT AGA GAA AAA ACA 1620
L K A A L H S L E T S Y P E L F R E K T
GAT AGT AAA AAG AAA CAA ATA AAT CTT AAT ATA TTT AAA TCT AAT CAA AAG ACC AAA TAT 1680
D S K K K E I N L N I F K S N E K T K Y
TTT TTA CAT CTT TCT CCG CCA ACT CCA CCG CCG CCG CCG CCG CCG CCG CCG CCG CCG 1740
F L D L S G C T A D L K K F V E R Y K N
AAT TAT CCG TCT TAT TAT CCG TCT CTT CCA AAA CAG CCA GTC ATT ATG CTT CTT GAT AAT 1800
N Y A S Y Y G S V P K Q P V I H V L D N
GAT ACA CCG CCA ACC GAT TTA CTT AAT TTT CTC CCG AAT AAA CTT AAA ACC TCG CCA GAC 1860
D T G P S D L L N F L R N K V K S C P D
GAT CTA ACT GAA ATG AGA AAG ATC AAA TAT ATT CAT CTT TTC TAT AAT TTA TAT ATA CTT 1920
D V T E H R K N K Y I H V F Y N L Y I V
CTC ACA CCA TTG ACT CCG TCG CCG CAA CAA ACT TCA ATC GAG GAT CTT TTC CCG AAA GAT 1980
L T P L S P S G E Q T S H E D L F P K D
ATT TTA CAT ATC AAG ATT CAT CCG AAC AAA TTC AAC AAA AAT AAT GAT CCA GAC TCA AAA 2040
I L D I K I D G K K F N K N N D G D S K
AGC GAA TAT CCG AAG CAT ATT TTT TCG ATG ACC CTT CTT ACA GAT AAA AAG CCG AAA ATA 2100
T E Y G K H I F S M R V V R D K K R K I
GAT TTT AAG CCA TTT TCT TGT ATT TTT GAT CCG ATA AAA GAT ATA AAG CAA CAT TAT AAA 2160
D F K A P G C I F D A I K D I K E H Y K
TTA ATG TTA AAT ACC TAA TCA ACA CCG CTA ACC TTA TCA ACC CTA ACC CTC ATT TTT CCG 2220
L H L N S
TAA AAT TTA TAT CCG TTG AAT TGT AAT ATA TTA TCT TCA ACC CAT TTA TTT AAT TCG TCG 2280
ATC CTT TTC TGT AAC CCG ATT AAT TCG TTC CTC ACA AAG ACT AAA CTC CCG TTT TCG ACA 2340
TCC CCA AAG CCG CCG AAT ATT ATT CCG CAT AAT CCG CAT CAT TTC CCG TCG CAC ACC ATG 2400
CGC TCG CAT CAT CTC ATC CCG CC

FIGURE 11

V	RT	VKLKPGMDGPKVKQ	WPLTEEKIKALVEICTEMEKEGKISKIGPENPYNTPVFAIKKKDSTKWR	239
LV1	RT	RPWARTPPKAPRNQ	PVPFKPERLQALQHLVRKALEAGHIEPYTG PGNNPVFPVKKA NGTWR	75
DNA	RT	NVLYRIGSDNQYTQFTIPKKGKGVRTISAPDRL	KDIQRRICDLLSDCRDEIFAIRKI SNNYS	94
		+ ○ ● ● ○	+ ●++ ● +	
V	RT	KLVDFRELNKRTQDFWEVQLGIPHPAGLKKK	KSVTVLDVGDAYFSVPLDEDFRKYTAFTIP SI	302
LV1	RT	FIHDLRATNSLTIDLSSSSPGPPDLSSLPTTLAHLQ	TIDLRLDAFFQIPLPKQFQPYFAFTVP QQ	139
DNA	RT	FGFE RGKSIILNAYKHRGKQIILNIDLKDFEF	SFNFGRVRG YFLS NQDF LLN PVVA	150
		○ ● + ●+ + +○ +● +● ●		
V	RT	NNETPGIRYQYNVLPQGWKGSPAIFQS	SMTKILEPFKKQNPDIVIYQYMDLLYVGS DLEIG	363
LV1	RT	CNYGPGTRYAWKVLPQGFKNSTPLFEM	QLAHILQPIRQAFPOCTILOYMDILLAS PSHE	199
DNA	RT	TTLAKAACYN GTLPQGSPIISNLICNIMDMRLAKLAKKY	GCTYSRYADDITI STNKNTF	212
		● ●●● ●● + + ○ + ○○ ●●● ●		
V	RT	QHRTKIEELRQHLLRWGLTTP	DKKHQKEP PFLWMGYELHPDKWTVQPIVLPE KDSWTVNDI	424
LV1	RT	DLLLLSEATMASLISHGLPVS	ENKTQQTPTGIKFLGQIISP NHLTYDAVPTVPI RSRWALPEL	262
DNA	RT	PLEMATVQPEGVVLGKVLVKEIENSGFEINDSKTRLTYKTSRQEV	T GLTVNRIVNIDRCYYKKT	276
		○ + ● ○○ ○ + ○ ● + +○		
V	RT	QKLVGKLNWASQIYPGIK	VRQLCKLLRGTKALTEVIPLTEEALELAENREILKEPVHGVYYD	487
LV1	RT	QALLGEIQWVSKGTPTLRQPLHSLYCALQRHTDPRDQIYLNPSQVQSLVQLRQALSQNCRSRLVQ		327
DNA	RT	RALAHALYRTGE YKVPDE NGV	LVSGLDKLEGMFGFIDQVDKFNNIKKLKNQ PDRYVL	335
		○● + + + + ○ + ○○ ● ○+○		
V	RT	PSKDLIA EIQKQGQGWTYQIYQE	PFKNLKTGKYARMRGAHTNDVKQLTEAVQKITT	544
LV1	RT	TLPLLGAIMLTLTGTTTVFQSKEQWPLVWLHAPLPHTSQCPWGQLLASAVLLLDKYTLQSY	GL	391
DNA	RT	TNATLHGFKLKL NAREKAY SKFIY YKFFHGNTCPTIITEGKTDRIVYLKAALHSLET	SYPEL	396
		○ ● ○○ + ○○ + ○ ○ + + +○ + ○○ ○		
V	RT	ESIVIWGKTPKFKLPIQKETWETWWTEYWQATWI	PE WEFV NTPPL VKLWYQ	595
LV1	RT	LCQTIHNNISTQTFNQFIQTSDHPSVPILLHSHRFRKNLGAQTGELWNTFLKTAAPLAPVKALMP		456
DNA	RT	FREKTDSKKKEINLNIFKSNEKTKYFLDLSGGTADLKKFVERYKNNYASYGVS	PKQPVIMVLD	460
		+ + ○○ + ○ ○	● ○●	
V	RT	LE KEPIV	GAETFYVDGAANRETKLGKAGYVTNKGRQK VV PLTNTTNQ KTELQAIYLA	652
LV1	RT	VFTLSP VIINTAPCLFSDGSTSRAAYILWDKQILSQRS	FP LPPPHKSA Q RAELLGLLHGL	516
DNA	RT	NDTG PSDLLN FLRNKVKSCPDVTEMRKMKYIHVFYNLYIVLTPLSPSGEQTSMEDLFPKDIL		523
		○ ● ○ + + + ○+○ +○ ●+ ○ ● ○ ● ○		
V	RT	LQDS GLE	VNIVTDSQYAL QIIQA QPDKSESELVNQIIEQLIKKEKVYLAWVPAHKG	708
LV1	RT	SSAR SWR CLNIFLDSKYLYHYLRTLALGTFQGRSSQAPFQA	LLPRLLSRKVVYLHHVRSHTN	578
DNA	RT	DIKIDGKKFNKNNDGDSKTEYGKHI	FSMR VV RDKKRKIDFKAFCCIFDA	572
		+ ● ●●○ ○ + ○ ○ ○ +○ +		
V	RT	IGGNEQVDKLVSAG		722
LV1	RT	LPDPISRLNALTDA		592
DNA	RT	IKDIKEHYKLMLNS		586
		+ ○ ++		

FIGURE 12

00000001-000000

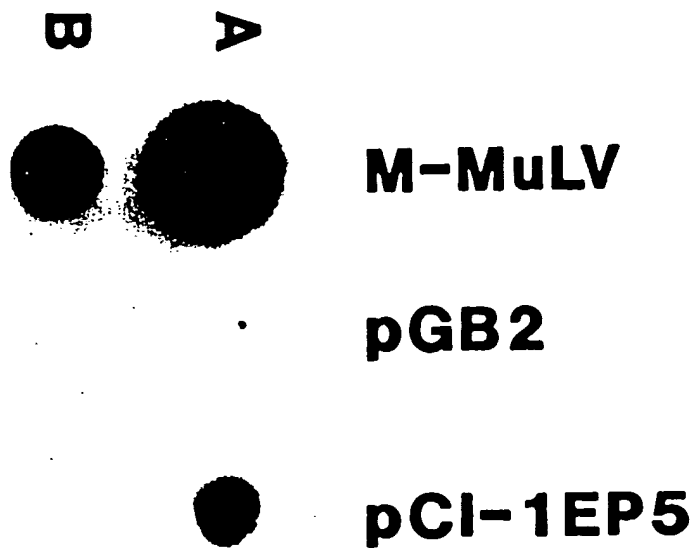


FIGURE 13

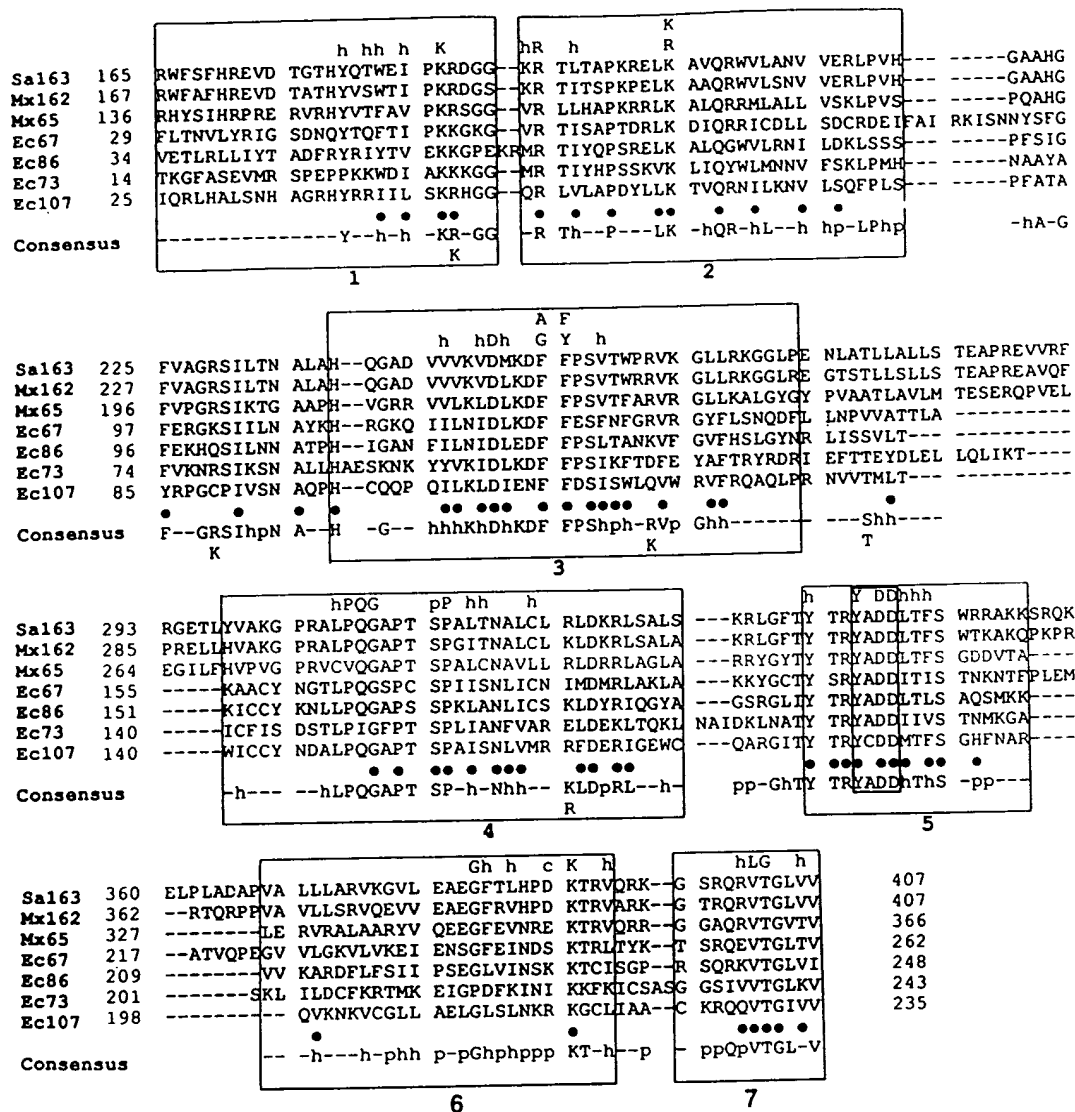


FIGURE 14

GCGCCGCTCCGAGGACGGCTCGCGCCCGGGCGGGCGGGCGGCGG 60
 CCGCCGACCGAGAGCGTTGACCCGGGAGACGAATGACGATAACGGCAGGTGCTC 120
 32 RNA
 CGGAGAGCCAGCGCTCGCACATGACATAGTACCGCGGTCTTTCCCGCGGGGTGT 180
 CCCTCTCCGTCGCGAGCGCTACTCGGTACTCATGGCGGCACAAAGCGGGCGGCGCA
 TCTGTCCCATCTCTTCCGACGGTCCGAGCGTACGGAACGACGGAGCCCGGCTCAA 240
 AGACAAGCGGTAGAGAAGCGGTCCGAGGCTCGCATGCGTTCGCTCCGCGGCGCAGGTT
 31 A1u1
 CGCCTCGCAGGTCTGCTCCCTGCGCTTTCCGGAGCACCATGAGTGGTTCGACACACCC 300
 CCGGACCGTCCAGCAGCGCACCGGAGAAGCGCTCGTGTACTCGACCAAGCTGTGGTGGG
 DNA H S V F D T T L
 TCTCCGCGCTCAAGCGGTGTTCAGCGCTCCGCTGACACGAAGCACCACCGGCTGCAGC 360
 S R L K G L F S R P V T R S T T G L D V
 TCCCGCTGCATGCCACGACGTCGCCAGGACGTCGTGACGGACACGCTCTCCAGCTCGG 420
 P L D A H G R P Q D V V T E T V S T S G
 CCGCCCTGAAGCCAGCGGACCTGGGACAGGTCCGCGGGATGCGCGGCTGCTCCCAAGG 480
 P L K P G H L R Q V R R D A R L L P K G
 CGGTCCGCGCTACACCCCGCGCGGAAGAAGTGGATGGAGCGCGCGCAAGCGCGCGCGC 540
 V R R Y T P G R K K W H E A A E A R R L
 TGTCTCCGCGACGCTGCGCACCGGGAACCGGAACCTGAGGACTTGTCCCGACGAGG 600
 F S A T L R T R N R N L R D L L P D E A
 CACAGCTGCGCGCTACGCGCTGCGGCTGTCGGCGCACGGAAGAGGACGTGCGCAGCGGCC 660
 Q L A R Y G L P V W R T E E D V A A A L
 TGGCGCTCTCGGTGCGCGTCTCGGCACTACAGCATCCACCGCGCGCGGAGCGGCTGC 720
 G V S V G V L R H Y S I H R P R E R V R
 GGCAGTACGTGACCTTCGCGCTGCCAAGCGCTCCGAGCGCTCCGCTGCTGCATGCGC 780
 H Y V T F A V P K R S G G V R L L H A P
 CCAAGCGCGCGCTGAAGCGCTGCCAAGCGGATGCTGCGCGCTCTGCTGCTGAAGCTCC 840
 K R R L K A L Q R R M L A L L V S K L P
 CGGTAGTCCACAGGCCATGCGTTCGTGCGCGCGGCTCCATCAAGACGGCGCGCGCGC 900
 V S P Q A H G F V P G R S I K T G A A P
 CGCAGCTGCGCGCGCGGTGCTCTGAAGCTGGAACCTGAAGGACTTCTTCCCTCCGTCA 960
 H V G R R V V L K L D L K D F F P S V T
 CTTTCCGCGCGGTGCGAGGCGTCTCATCGCGCTGCGCTACGCTATCCGCTGCGCGGCA 1020
 F A R V R G L L I A L G Y G Y P V A A T
 CGCTCCGCGTCTGATGACGAGTCCGAGCGCGCAGCGCTGGAGCTGGAGGGATCCTCT 1080
 L A V L M T E S E R Q P V E L E G I L F
 TCCAGCTTCCGCTGCGCGCACCGCTCTGCGTGCAGGGCGCGCGCACGAGCGCGCGCTGT 1140
 H V P V G P R V C V Q G A P T S P A L C
 GCAACGCGCTGCTGCTGCGACTGACCGCGCGGTGCGCGGACTGCGCGCTCGGTACGGCT 1200
 N A V L L R L D R R L A G L A R R Y G Y
 ACAGCTACCGCGCTACGCGATGACCTCACCTTCTCGCGGACGACGTACGCGCGCTCG 1260
 T Y T R Y A D D L T F S G D D V T A L E
 AGCGACTCCGCGCGTCCGCGCGGTAAGTGCAGGAGGAAGGCTTCAGCTCAACCGCG 1320
 R V R A L A A R Y V Q E E G F E V N R E
 AGAAGACCGCGTGCAGCGCGCGCGGCTGCCACGCGCTCACTGCGCTACCGTGAATA 1380
 K T R V Q R R G G A Q R V T G V T V N T
 CGACGCTCGGCTTGTACGCGAGGAGCGCGCGGCTCGCGCGATGCTGCACGAGGAG 1440
 T L G L S R E E R P R L R A M L H Q E A
 CGCGGTGCGAGGACGTGAGGCACACCGCGGACCTCGACGCGCTCTGCGCTACGTGA 1500
 R S E D V E A H R A H L D G L L A Y V K
 AGATGCTCAAGCGGAGCAGCGGAGCGGCTCGCTCGCGCGCGCAAGCGCGCGCGACCT 1560
 M L N P E Q A E R L A R R R K P R G T *
 GAGCGAGGCTCAGTCCGATGCGCGAGGCGCTGTACGCGTCCGCGCTCCAGTTGT 1620
 CATGCGCGCGCTCCAGTAC

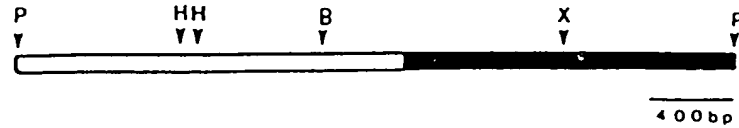
FIGURE 15

CC ACT TCC GGC GCT CGG GCT GCG GGA GGG CCC GTG GGA GCA CAT GAT GGC GCT GCG GCT 60
 GT CCA GGT CGG GCA CGC CGC GGA GCA GGA AGC ACT GCG TCA GAC CCC CGC GGG CGG CCA 120
 CT CAT CGG CGC GGA GAC CGC CTC CTA GGT GCG GCG GGA GGC CTC CGG CCA GGA GCA GGT 180
 TA CGG GGT CTC ATT GGA TGG GAA AGT GGT GCG GGT GGA GTG GGG CCC CGG CCA GGG GGA 240
 TC CGG CGG GGA GAA GGT CTC GTT GGA CAC GGA CGC GGA GGC CGC CAC CGC CTA CTT CAC 300
 TG CTT GGA GTC CTT GCG CGC GGA GGG ATA TAT GGA TGC GGC TGC TTC AAT GAT GTA GAA 360
 AC GCA AGC CAC CGG CGC CGC GCG CGG CGG AAA CGC AGC TGC CAC GGA AGC ACA GAC 420
 31 RNA< 1
 TT CGT GCG AGC GAC CCA GAG AGC TCC CAA GCG ATC AGC CTC AGC GCG TCG AGC GCG AGA 480
 TA GCA CGC TCG CTC GCT CTC TCC AGC GTT CGG TAG TCG GAG TCG CGG AGC TCG CGC TCT
 TG GCG TTG CGC CGC TCT GGT TGA ATT GGA GGA CAC TCT CGG CAA GGT AGC CTG TTC TTG 540
 TC CGC AAC CGG CGC GGA CCA ACT TAA GGT GGT GTG AGA GGC GTT CCA TCG GAC AAG AAG
 T CTC TTC CTT CGG GTG AGT ACC TCT CGG CGC GCG GAG CTG AAC CAA GGA CGC AAC CGC 600
 A GAG AAG GGA GGC CAC TCA TGG AGA GGC CGC CGC CTC GAG TTG GTT GCT GCG TTG GCG
 TT TTC CGC CGC CGC AGA GGT ACT CAC CGG AGC GGA GAG CGC CTG AGC CTA CGC TCC CGC 660
 A AAG GCG CGC CGC TCT CCA TGA GTG GCG TCC CTT CTC GCG CAC TCG GAT GCG AGC GCG
 31
 TG TGA GAA GGT GGT GCG TTC GCG CTT CGC TCG AGC GCT CGC GCT CGC TCG CGC TCG CCA 720
 TC AGT GGT GGA CCA CGG AAG CGC GGA GCG AGC TCG GGA GCG CGA GCG AGC GCG AGC GCG
 CG TCG CGC CGC CCA CTT TCG TCA CGG GCG CCA GGA GCG GTC ATG AGC GCG AAG CTG GAG 780
 CA CAC GTC CGC GCG GCG CGC CGC GTC TCG GCG GCG GCG CGC CGC CGC ACC GGT CGC GAT 840
 TC GCG AAG CAG GAG GCG CGC CGC GCG CAC CAC GAG GCG CTG CGC CTG CGG TCG AAG GCG 900
 TC GAA GAG GCG GCG GCG AGC GAC GCG TCG GTG CGG CAG CAG CTG GTG GCG AAG GCG GTC 960
 TC GCG GCG GAG GAG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG 1020
 AG AAG AAG GCG GCG GCG ACC GAG CGC CGC GCG CAG AAG CGC CTG GCG TCG GAG GCG TCG 1080
 AG GCG AAG CAC ATC CAC CAC CTG GCG GTG GCG GTG CAC TCG GAG GAG GCG GCG GCG GCG 1140
 AC AAG TTC GAC GTG GCG GCG GCG GAG GAG GCG GCG AAG GCG AAG GCG TTC CGG GAG GCG 1200
 TG CAC TCG GTC GAG GCG CTG GCG AAA GCG CTG GCG ATC TCG GTG TCG CGC CTG CGC TCG 1260
 TC TCG TTC CAC CGC GAG GTG GAC AGC GCG AGC CAC TAC CAG AGC TCG GAG ATT CGG AAG 1320
 CG GAC GCG GCG AAG CGG AGC CTC ACC GCG CGG AAG CGG GAG CTC AAG GCG GTG CAG CGC 1380
 CG GTC GCG AAG GTG GTG GAG CGG CTG CGG GTG CAC GCG GCG GCG CAC GCG TTC GTG 1440
 CGG GCG CGC TCC ATC CTC ACC AAC CGC CTG GCG CAC CAG CGC CGC GAG GTC GTG AAG 1500
 A G R S I L T N A L A H Q G C A D V V V K
 GTG GAC ATG AAG GAC TTC TTC CCT TCC CTG AGC TCG CGC CGG GTC AAG GGA CTG CTG CGC 1560
 V D N K D F F P S V T W P R V K G L L R
 250
 AAG GGA GGA CTC CGG GAG AAC CTG GCG AGC CTC GCG CTG CTC TCC ACC GAG GCG CGC 1620
 K G C L P E N L A T L L A L L S T E A P
 CGC CAG GTG GTG CGG TTC CGG GGA GAG AGC CTG TAC GTG GCG AAG GCG CCG CGC CGC CTG 1680
 R E V V R F R G E T L Y V A K G F R A L
 CGC CAG GCG CGC CGC ACC TCT CGG CGC CTG AGC AAC GCG CTG TCG CGG CTG GAG AAG 1740
 P Q G A P T S P A L T N A C L C L R L D K
 300
 CGG CTC TCG CGG CTG TCG AAG CGG CTG GCG TTC AGC TAC AGC CGC TAT GCG GAT CAC CTG 1800
 R L S A L S K R L G F T Y T R V A D B L
 ACG TTC TCC TCG CGG CGG AAG AAG TCC CGG CAG AAG GAA CTC CGC CTG GCG GAT GCG 1860
 T F S M R R A K K S R Q K E L P L A D A
 350
 CGG GTG GCG CTG CTG CTG GCG GCG GTG AAG GGT GTG CTG GAG GCG GAG GGT TTC AGC CTG 1920
 P V A L L L A R V K G V L E A E G F T L
 CAC CGG GAG AAG AGC CGG GTG CAG CGC AAG GCG AGC CGG CAG GCG GTC AGC GCG CTG GTG 1980
 H P D K T R V Q R K G S R Q K E L P L A D A
 400
 CTG AAC GAG GCG CGC GAG GCG GTT CGG GGT GCG CGG GTG CGC CGC GAT GTG GTG CGG CGG 2040
 V M E A P E G V P G A R V P R D V V R R
 CTG CGC GCG GCG ATC CAC AAG CGG GAG CAG GCG AAG CGC GCG CGC CGC CGC CGC CGC 2100
 L R A A I H M R E Q G K P G P T G E T L
 GAG CAG CTC AAG GCG CTC GCG GCG TTC CTT CAC ATG AGC GAG GCG AAG GCG CGC GCG 2160
 E Q L K G L A A F L H M T D A E K G R A
 450
 TTC CTG CGA CGG CTG GAG GCG CTC GAG AAG CGC CAG ACC GCG TGA CGC TCA CTG GTC GTC 2220
 F L R R L E A L E K R Q T A -
 CGG GCG ATC GCA GCG GCG GCG AGC GAG CGT CAC CGC CCA GAT CTC CAT GCG ATC CTG 2280
 GGG ATT CTG GCG GGT GAA GAA GAC TTC CCA GCG GAG AGC GAA GCG CTG CGG ATC CGA 2340
 TGA CTC CTC CGC CGC GAT CTC CGG GAG GCG CAC GGT TCC GAC CTC GGT GCG ATT GCT 2400
 CAC CCA GCG GTC CGC GCG CCA GCG ATC CTC GCG GCG CGC CGC CAA ATC CTT CAG CAG CAG 2460
 GCG CGT CAG GGT GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG 2520
 GGT GCG CTT GCG GGT GCG ATC GCT GGA CCA CAG CTC CGC GCG GTG GAG GCT GTC ACT CGC 2580
 GCG GAA GTA GAG CAT CGC ATT CAG CGC CTT GAT GCG GCT GCG GCG CGA GCT GTC CGG ACC 2640
 CGG CCA GAT GTC CTT CAC CGC GAG CGT GCG ATG CGA CGT GCG ATC GCT GAC CCA CAG CTC 2700
 CTC GCG CTC GCG CTG GCG CCA GAA CTC GCG CTC GCG TCC CGC GCG GCT GAA GAA GAT CTT 2760
 CGC CGC GAG CGC GGT GAG ATC ATG CGG ATA GAG GCG GCG GAA GAA GCG CAG CTG CTC GGA 2820
 GAG GGT GCG TCT GGA GCA CCA CAG GGT GCG CTC GCG TTC GTC ATT GTC GAG CAG GAA GAA 2880
 GAG CAC GGA GTC CGC CGC GGT GAA CGC GGA GAG GAA GTT GTC CTC CGC CGC GGT GAA GAG 2940
 AGA GGT GGT GGT GGA CAG CGC CAG GGT GCG CCA GAT GAA CAC CTC GTC ATT GAG GTT GCG 3000
 CAC GAA GAA GAG CGC ATC GCG CAG CGG GGT GAG CGG GCG GCG GGT GGA GCT GCG GCG CAG 3060

FIGURE 16

FIGURE 17

(A)



-371 TGGCATCTATTAAAGAGGTTAGGAAAGAAAAATAAGTATCAAAAGATATTGGAAATATAT
-311 TATACGCAGAGCGTTTCTATTGCCCTGTATCTATTTACTGGATAGTGCAACTACCGCAC
-251 ACTGTGTGAAGTAGCTTTTAAAGCGATAAAGCAAGATGATGTTTTATCTAAAAATTATTGT
-191 TAGATCCGTTGTTTCTCGTCTAATAAATGAACGAAAAATACITCAAATGACTGATGGTTA
-131 TCAGGTCACCTGCTTTGGGGGCTAGCTATGTTAGGAGCGCTTTTGATAGAAAGACACTTGA
-71 CCGATTGGCGCTTGAGATTATGAATTTTGAAAACCGTAGAAAAATCAACATTTAACTATGA
-11 TAAGATTCCGATATGCGCACCTTAGCGAGAGGTTTATCATTAAAGGTCAACCTCTGGATGT
IR -----
49 TGTTCGGCATCTGCAATTGAATCTGAGTTACTGTCTGTTTTCTTGTGGAAACGGAGAG

109 CATCGCTGATGCTCTCCGAGCCAACCGAAACCCGTTTTTCTGACGTAAGGGTGCGC

169 AACTTTCATGAAATCCGCTGAATATTGAACACTTTTAGATTGAGAAATCTCGGCTACC
- IR MetLysSerAlaGluTyrLeuAsnThrPheArgLeuArgAsnLeuGlyLeuPr
229 TGTCATGAACAATTTGCATGACATGTCTAAGGCGACTCGCATATCTGTTGAAACACTTCG
ovalMetAsnAsnLeuHisAspMetSerLysAlaThrArgIleSerValGluThrLeuAr
289 GTTGTTAATCTATACAGCTGATTTTCGCTATAGGATCTACACTGTAGAAAAAGAGGCC
gLeuLeuIleTyrThrAlaAspPheArgTyrArgIleTyrThrValGluLysLysGlyPr
349 AGAGAAGAGAATGAGAACCATTACCAACCTTCTCGAGAACTAAAGCCTTACAAGGATG
oGluLysArgMetArgThrIleTyrGlnProSerArgGluLeuLysAlaLeuGlnGlyTr
409 GGTCTACGTAACATTTTAGATAAACTGTCGTCATCTCTTTTCTATTGGATTGAAAA
pValLeuArgAsnIleLeuAspLysLeuSerSerSerProPheSerIleGlyPheGluLy
469 GCACCAATCTATTTGAATAATGCTACCCCGCATATTGGGGCAAACTTTATACTGAATAT
shisGlnSerIleLeuAsnAsnAlaThrProHisIleGlyAlaAsnPheIleLeuAsnI
529 TGATTGGAGGATTTTCCCAAGTTAACTGCTAACAAAGTTTTGGAGTGTTCATTTC
eAspLeuGluAspPhePheProSerLeuThrAlaAsnLysValPheGlyValPheHisSe
589 TCTTGGTTATAATCGACTAATATCTTCAGTTTGGACAAAAATATGTTGTTAAAAATCT
rLeuGlyTyrAsnArgLeuIleSerSerValLeuThrLysIleCysCysTyrLysAsnLe
649 GCTACCACAAGGTGCTCCATCATCACCTAAATTAGCTAATCTAATATGTTCTAAACTTGA
uLeuProGlnGlyAlaProSerSerProLysLeuAlaAsnLeuIleCysSerLysLeuAs
709 TTATCGTATTTCAGGGTTATGCAGGTAGTCGGGGCTTGATATATACGAGATATGCCGATGA
pTyrArgIleGlnGlyTyrAlaGlySerArgGlyLeuIleTyrThrArgTyrAlaAspAs
769 TCTCACCTTATCTGCACAGTCTATGAAAAGGTTGTTAAGCACGTGATTTTTTATTTTC
pLeuThrLeuSerAlaGlnSerMetLysLysValValLysAlaArgAspPheLeuPheSe
829 TATAATCCCAAGTGAAGGATTGGTTATTAACCAAAAAAATGTTATTAGTGGGCTCG
rIleIleProSerGluGlyLeuValIleAsnSerLysLysThrCysIleSerGlyProAr
889 TAGTCAGAGGAAAGTTACAGGTTTAGTTATTTACAAAGAGAAAGTTGGGATAGGTAGAGA
qSerGlnArgLysValThrGlyLeuValIleSerGlnGluLysValGlyIleGlyArgGl
949 AAAATATAAGAAATTAGAGCAAGATACATCATATTTTCCGGTAAGTCTTCTGAGAT
uLysTyrLysGluIleArgAlaLysIleHisHisIlePheCysGlyLysSerSerGluIl
1009 AGAACACGTTACGGGATGGTTGTCATTTATTTAAGTGTGGATTCAAAAAGCCATAGGAG
eGluHisValArgGlyTrpLeuSerPheIleLeuSerValAspSerLysSerHisArgAr
1069 ATTAATAACTTATATTAGCAAATTAGAAAAAAATATGGAAGAACCTTTAAATAAAGC
qLeuIleThrTyrIleSerLysLeuGluLysLysTyrGlyLysAsnProLeuAsnLysAl
1129 GAAGACCTAATGGTCTTCGTTTTAAACTAAAGCTCATAGGTTGAAAAATTGAGCACTTC
aLysThr
1189 TTCGTCCAACAGTTATTTAGTTCCTGCAATCGTTTCTGCAG

FIGURE 18

0303031-030397

Oligo 2337
 tcaccctgaaagacctgattgcttacctggaagagaagccggaatgcggaacatctgg 60
 cggcggttaaggcctatcgcaagagttcggcggtttaaaAATATGCGCTGTCAGGCTTT 120
 TTGCTGTCGCGCAGCGTGATGCGCTTCAAGATATCGTGTAAATCTGCTTTGCCAGCAGTG 180
 AACGACACCGCTCGCACTACGCGAAGTTCTATAGCAAAATAGACGAAAGCGGTCGTCAC
 GCAATAGCGTTTCCGGCCTTTTGTGCGGGAGGGTCGGCGAGTCGCTGACTTAACGCCAG 240
 CGTTATCGCAAAGGCCGAAAACACGGCCCTCCAGCCGCTCAGCGACTGAATTGCGGTC
 TAGTATGTCCATATACCCAAAGTCGCTTCATTGTACCTGAGTACGCTTCGCGTACGTCGC 300
 ATCATACAGGTATATGGGTTTCAGCGAAGTAACATGGACTCATGCGAAGCGCATGCCAGCG
 GCTGACGCGCTCAGTACAGTTACGCGCCTTCGGGATGGTTTAAATGGTATTGCCGCTGTTG 360
 CGACTGCGCGAGTCATGTCAATGCGCGGAAGCCCTACCAAATTAACATAACGCGGACAAC
 GCGCCTCTTTTGGCCGCGTGATGTGGAGAGTGAATGGATGCTACCCGGACAACCCCTTC 420
 M D A T R T T L L
 TGGCGCTCGATTGTTCGGCTCGCCGGGCTGGAGCGCGGATAAAGAAATACAGCGACTGC 480
 A L D L F G S P G W S A D K E I Q R L H
 ATGCGCTCAGTAATCATGCCGAGCCATTACCGACGCATTATCTTTCTAAACGCCACG 540
 A L S N H A G R H Y R R I I L S K R H G
 GTGGTCAGCGCTGGTGTAGCCCTGATTACTTGCTCAAAACCGTACAGCGCAACATTC 600
 G Q R L V L A P D Y L L K T V Q R N I L
 TTAAGAACGTCTTTTCAATTTCCGCTTTCCCTTTTGTCTACAGCCTACCGACCAGTT 660
 K N V L S Q F P L S P F A T A Y R P G C
 GCCCAATCGTCAGCAACCGCGAGCCACACTGCCAACAGCCGAGATCCTGAAACTCGATA 720
 P I V S N A Q P H C Q Q P Q I L K L D I
 TCGAAAACCTTTTTCGATAGCATTAGCTGGTTACAGGTCTGGCGTGTGTTTCGCCAGGCC 780
 E N F F D S I S W L Q V W R V F R Q A Q
 AGTTGCCACGTAATGTGGTAACCATGCTGACCTGGATTGTTGTTATAACGACGCGTTAC 840
 L P R N V V T M L T W I C C Y N D A L P
 CGCAGGGGGCACCAACTTCGCCAGCCATTTCGAATCTTGTGATGCGCCGTTTGTATGAAC 900
 Q G A P T S P A I S N L V M R R F D E R
 GCATAGGGGAATGGTGTGAGGCTCGGGGAATTACCTACACCCGCTACTGCGATGACATGA 960
 I G E W C Q A R G I T Y T R Y C D D M T
 CCTTTTCAGGTCACCTTCAATGCCCGCAGGTAAAAATAAAGTGTGCGGATTGTTAGCGG 1020
 F S G H F N A R Q V K N K V C G L L A E
 AGCTGGGCCTGAGCCTCAATAAACGCAAAGGCTGCCTGATAGCTGCCTGTAAGCGCCAGC 1080
 L G L S L N K R K G C L I A A C K R Q Q
 AAGTAACCGGGATTGTTGTTAATCACAAGCCACAGCTTGCCCGTGAAGCGCGCGGGGCGC 1140
 V T G I V V N H K P Q L A R E A R R A L
 TGGCTCAGGAGGTGCATTGTGCCAAAATATGGCGTTATTTTCGCATCTTAGTCATCGTG 1200
 R Q E V H L C Q K Y G V I S H L S H R G
 GTGAACTTGATCCTTCTGGCGATCTCCACGCACAGGCAACGGCGTATCTTTATGCTTTGC 1260
 E L D P S G D L H A Q A T A Y L Y A L Q
 AGGGAAGAATAAACTGGTTATTGCAAATCAACCTGAGGATGAGGCTTTCAACAGGCGA 1320
 G R I N W L L Q I N P E D E A F Q Q A R
 GAGAGAGTGTAAGCGAATGCTGGTTGCATGGTAAGAAAAGCGTCAGGCAGACGTTTCTG 1380
 E S V K R M L V A W *
 CCTGACCGTTTAGGGGAGAattactgcaactgcgcggaattagcggccagcggcggtca 1440
 aaatcatcgtcgggcggtatttaaaactcgctgcggaacaaacgtgacagcataccttca 1500
 cagaaggccagatctggcttgccagcaggggttcatcgg 1540
 Oligo 2336

FIGURE 19

26E0E0-TE0B0B20

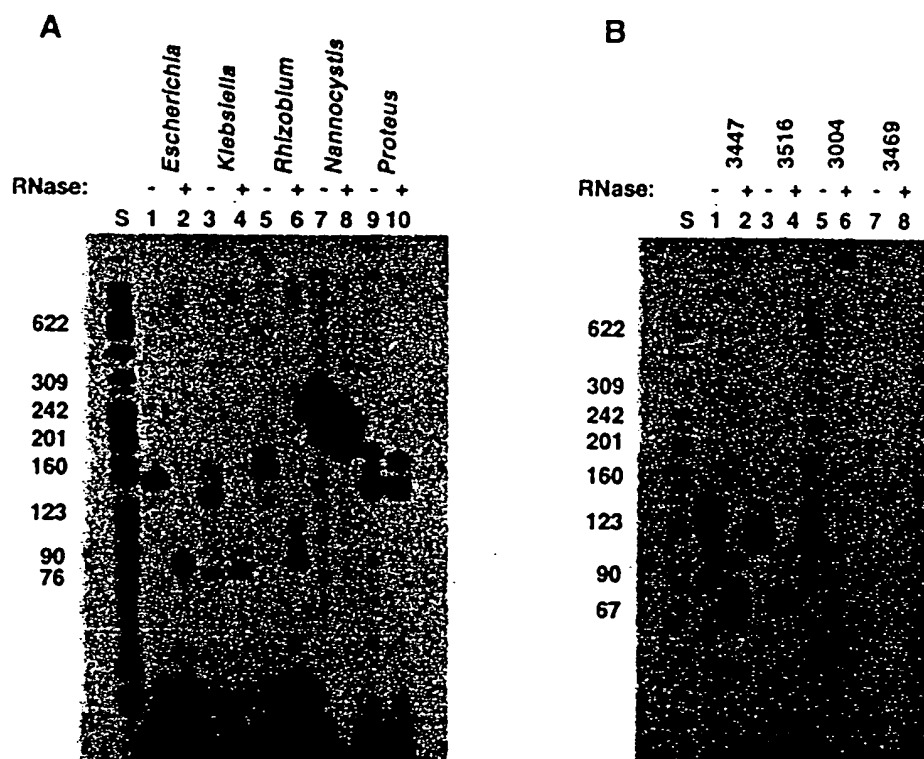


FIGURE 20

RHIZOBIAL ISOLATES

Strain (legume host genus)	USDA strain no.	Geographic source (date)	msDNA produced ^b
<i>Rhizobium</i> sp. (<i>Acacia</i>)	3002	Brazil (1959)	+
	3003	Africa (1950)	
	3325	Morocco (1974)	
	3838	? (1976)	
<i>Bradyrhizobium</i> sp. (<i>Aeschynomene</i>)	3516	Florida (1972)	+
	4362		+
<i>Bradyrhizobium</i> sp. (<i>Albizia</i>)	3004	Maryland (1952)	+
<i>Bradyrhizobium</i> sp. (<i>Apios</i>)	3240	Maryland (1939)	
<i>Bradyrhizobium</i> sp. (<i>Arachis</i>)	3339	Thailand (1979)	
	3341	Hawaii (1978)	
<i>Rhizobium</i> sp. (<i>Astragalus</i>)	3854	Alaska (1962)	
<i>Rhizobium</i> sp. (<i>Cajanus</i>)	3472		
<i>Bradyrhizobium</i> sp. (<i>Canavalia</i>)	3317	Brazil (1974)	
<i>Rhizobium</i> sp. (<i>Cicer</i>)	3378		
	3379	Mexico (1963)	
<i>Bradyrhizobium</i> sp. (<i>Coronilla</i>)	3165	Virginia (1935)	
	3167	? (1961)	
<i>Bradyrhizobium</i> sp. (<i>Crotalaria</i>)	3384	Brazil (1967)	
<i>Bradyrhizobium</i> sp. (<i>Desmodium</i>)	3225	Ecuador (1948)	
<i>Bradyrhizobium</i> sp. (<i>Erythrina</i>)	3241		
	3242	Maryland (1939)	+
<i>Rhizobium fredii</i>	191	China (1979)	
<i>Rhizobium leguminosarum</i>	2370	Illinois (1933)	
	2429	Hawaii (1978)	
	2435	Holland (1955)	
	2480	Tennessee (1951)	
	2489		
<i>Rhizobium</i> sp. (<i>Lens</i>)	2426		
	3404	Colombia (1979)	
<i>Rhizobium loti</i>	3084	Maryland (1946)	
	3468	New Zealand (1961)	+
	3469		
	3471		
	3503		
<i>Bradyrhizobium</i> sp. (<i>Lotus</i>)	3669	California (1968)	
	3074	Minnesota (1954)	
	3470	California (1916)	
<i>Rhizobium</i> sp. (<i>Lupinus</i>)	3040	Florida (1940)	
<i>Bradyrhizobium</i> sp. (<i>Lupinus</i>)	3045	Florida (1946)	
<i>Bradyrhizobium</i> sp. (<i>Macrotyloma</i>)	3451	Zimbabwe (1960)	
<i>Rhizobium medicago</i>	1097	North Dakota (1948)	
<i>Rhizobium meliloti</i>	1011	Maryland (1933)	
	1021a	North Dakota (1948)	
<i>Rhizobium phaseoli</i>	2667	Washington (1948)	
	2669		
	2674	Brazil (?)	
	2676	Colombia (1972)	
	3256	Illinois (1941)	
<i>Rhizobium</i> sp. (<i>Robinia</i>)	3436		
<i>Bradyrhizobium</i> sp. (<i>Stylosanthes</i>)	3441	Brazil (?)	
	3477	Colombia (1976)	
<i>Rhizobium trifolii</i>	2046	Virginia (1934)	
	2048	Illinois (1934)	+
	2063	Florida (1939)	
	2065	Alabama (1952)	
	2116	South Carolina (1944)	
	2134	? (1974)	
	2145		
	2156	California (1920)	
<i>Rhizobium</i> sp. (<i>Trigonella</i>)	1177	Florida (1939)	
<i>Rhizobium tropici</i>	2744	Brazil (?)	
<i>Bradyrhizobium</i> sp. (<i>Vigna</i>)	3447	Thailand (1979)	+
	3456	Wisconsin (1966)	

^a All strains are from the USDA Beltsville Rhizobium Culture Collection, provided by Peter van Berkum.

^b As defined by detection of radiolabeled msDNA by the RT extension method.